

09875324.060004
T090900-T252860

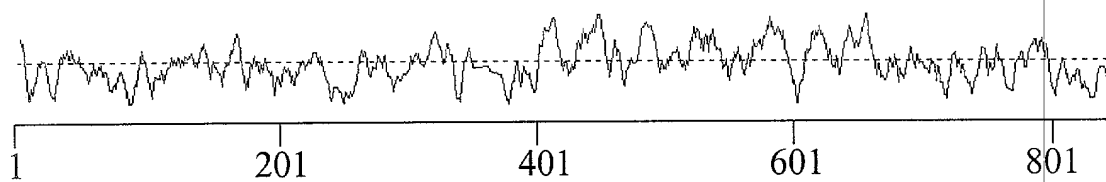


Figure 1

ion_trans: domain 1 of 1, from 472 to 661: score 0.1, E = 1.2
 (SEQ ID NO:9) *->ilfildllfvllfllleivlkfiayglkstsniaakylksifnildll
 ++ i + ++f++ ++l +++ ++ y +++ +
 52906 472 DWRIAMTYERIFFICLEILVCAIHPI-----PGNYTFTWTA-RLAF 511
 ailpllllllvflslgteqvakkrlrerfslelsqwyrylrlrllR
 ++ p+ + + + l++ +Lrl+
 52906 512 SYAPS--TTTADVDI-----LSIPMFLRLYL 536
 lLrllrllrrletlf.e.....fe.lgtlaWslqslgralksilrfllll
 + r++ ++ +lf+ ++++++ l ++ +k+++ ++ +
 52906 537 ---IARVMLLHSKLFtDtssrsIGaLNKI--NFNTRFVMKTLMTICPGT 580
 lllligfsvigyllfkgyedlsenevdgnsefssyfdafyflfvltttvG
 +ll++ s+ ++++ + + +e+ d+ + s++ a++ +t++++G
 52906 581 VLLVF--SISLWIIAAWTVRACERYHDQQDVTSNFLGAMWLISITFLSIG 628
 fGdlvpvwlgiiffvlfffiivgllllnlliavi<-*
 +Gd+vp++++ ++l+ i+g ++l +av+
 52906 629 YGDMVPNTYCGKGVCLLTGIMGAGCTALVVAVV 661

Figure 2

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09875321.060601

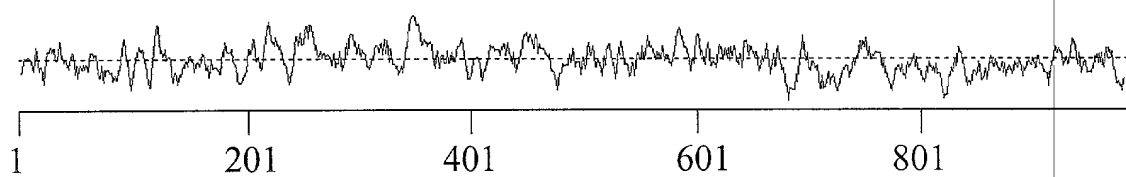


Figure 3

33408
rat EAG2
(SEQ ID NO:12)

MPGGKRGLVA PQNTFLENIV RRSSESSFLG GNAQIVDWPV VYSNDGFCKL
MPGGKRGLVA PQNTFLENIV RRSSESSFLG GNAQIVDWPV VYSNDGFCKL

SGYHRADV MQ KSSTCSFMYG ELTDKKTIEK VRQTFDNYES NCFEVLKYK
SGYHRADV MQ KSSTCSFMYG ELTDKKTIEK VRQTFDNYES NCFEVLKYK

NRTPVWFY MQ IAPIRNEHEK VVLFLCTFKD ITLTKQPIED DSTKGWTKFA
NRTPVWFY MQ IAPIRNEHEK VVLFLCTFKD ITLTKQPIED DSTKGWTKFA

RLTRALTNSR SVLQQLTMPN KTEVVHKHSR LAEVLQLGSD ILPQYKQEAP
RLTRALTNSR SVLQQLTMPN KTETVHKHSR LAEVLQLGSD ILPQYKQEAP

KTPPHIILHY CAFKTTWDWV ILILTFYTAI MVPYNVSFKT KQNNIAWLVL
KTPPHIILHY CAFKTTWDWV ILILTFYTAI MVPYNVSFKT KQNNIAWLVL

DSVVDVIFLV DIVLNFHTTF VGPGEVISED PKLIRMNYLK TWFVIDLLSC
DSVVDVIFLV DIVLNFHTTF VGPGEVISED PKLIRMNYLK TWFVIDLLSC

LPYDIINAFE NVDEGISSLF SSLKVVRLLR LGRVARKLDH YLEYGA AVL
LPYDIINAFE NVDEGISSLF SSLKVVRLLR LGRVARKLDH YLEYGA AVL

LLVCVFGLVA HWLACIWYSI GDYEVIDEVT NTIQIDSWLY QLALSIGTPY
LLVCVFGLVA HWLACIWYSI GDYEVIDEVT NTIQIDSWLY QLALSIRTPY

RYNTSAGIWE GGPSKDSLYV SSlyFTMTSL TTIGFGNIAP TTDVEKMFSV
RYNTSAGIWE GGPSKDSLYV SSlyFTMTSL TTIGFGNIAP TTDVEKMFSV

AMMMVGSLLY ATIFGNVTTI FQOMYANTNR YHEMLNNVRD FLKLYQVPKG
AMMMVGSLLY ATIFGNVTTI FQOMYANTNR YHEMLNNVRD FLKLYQVPKG

LSERVMDYIV STWSMSKGID TEKVL SICPK DMRADICVHL NRKVFNEHPA
LSERVMDYIV STWSMSKGID TEKVL SICPK DMRADICVHL NRKVFNEHPA

FRLASDGCLR ALAVEFQTIH CAPGD LIYHA GESVDALCFV VSGSLEVIQD
FRLASDGCLR ALAVEFQTIH CAPGD LIYHA GESVDALCFV VSGSLEVIQD

DEVVAILGKG DVFGDIFWKE TTLAHACANV RALTYCDLHI IKREALLKVL
EEVVAILGKG DVFGDIFWKE TTLAHACANV RALTYCDLHI IKREALLKVL

Figure 4C

09875321.060604

DFYTAFANSF	SRNLT LTCNL	RKRIIFRKIS	DVKKEEEEERL	RQKNEVTLSI
DFYTAFANSF	SRNLT LTCNL	RKRIIFRKIS	DVKKEEEEERL	RQKNEVTLSI
PVDHPVRKLF	QKFKQQKELR	NQGSTQGDPE	RNQLQVESRS	LQNGTSITGT
PVDHPVRKLF	QKFKQQKELR	NQGSAQSDPE	RSQLQVESRP	LQNGASITGT
SVVTVSQITP	IQTSLAYVKT	SESLKQNNRD	AMELKPNGGA	DQKCLKVNSP
SVVTVSQITP	IQTSLAYVKT	SETLKQNNRD	AMELKPNGGA	EPKCLKVNSP
IRMKNGNGKG	WLRLKNNMGA	HEEKEDWNN	VTKAESMGLL	SEDPKSSDSE
IRMKNGNGKG	WLRLKNNMGA	HEEKKEEWN	VTKAESMGLL	SEDPKGS DSE
NSVTKNPLRK	TDSCDSGITK	SDLRLDKAGE	ARSPLEHSPI	QADAKHPFYP
NSVTKNPLRK	TDSCDSGITK	SDLRLDKAGE	ARSPLEHSPS	QADAKHPFYP
IPEQALQTTL	QEVKHELKED	IQLLS CRM TA	LEKQVAEILK	ILSEKSVPQA
IPEQALQTTL	QEVKHELKED	IQLLS CRM TA	LEKQVAEILK	LLSEKSVPQT
SSPKSQMPLQ	VPPQIPCQDI	FSVSRPESPE	SDKDEIHF	
SSPKPQIPLQ	VPPQIPCQDI	FSVSRPESPE	SDKDEINF	

Figure 4D

09875331-050604

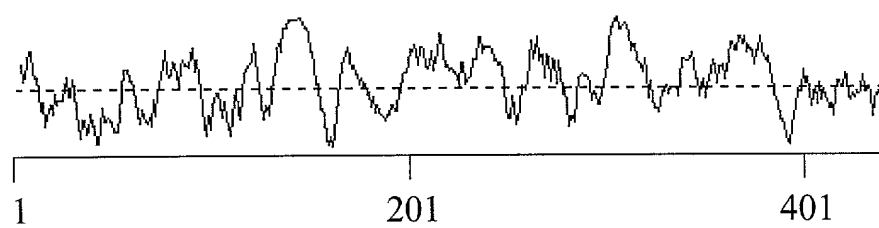


Figure 5

K_tetra: domain 1 of 1, from 3 to 101: score 169.0, E = 7.9e-47
 (SEQ ID NO:11) *->ErvrLNVGGkrFeTskstLtrfkpdTlLgrllktdsdvhearlrld
 Er++LNV G+rFeT+++TL rf pdTlLg++++ r ++
 12189 3 ERLVLNVAGLRFETRARTLGRF-PDTLLGDPAR-----R-GR 37
 fyddetgEyFFDRsPkhFetILnfYRtGdGkLhrp.evclidsfleEleFy
 fydd++ EyFFDR++++F+++L++Y++G G+L+rp +v+ld+fleE +Fy
 12189 38 FYDDARREYFFDRHRPSFDAVLYYYQSG-GRLRRPaHVPLDVFLEEVAFY 86
 gldelaiesCcedeY<-*
 gl+ a++ +ede+
 12189 87 GLGAAALARLREDEG 101

Figure 6A

ion_trans: domain 1 of 1, from 198 to 383: score 144.8, E = 1.5e-39
 (SEQ ID NO:9) *->ilfildllfvllflleivlkfiayglkstsniakylksifnildll
 ++f++++l++ +f +e++++ ++ k a ++k+++n++d+
 12189 198 PFFVETLCICWFSPELLVRLLCPSK-----AIFFKNVMLIDFV 238
 ailplllllvflsgteqvakkrlrerfslelsqwyrrilrflrlLrllR
 ailp+++ l+ l+++ +++++ +L +lR
 12189 239 AILPYFVALGTELARQ-----RGVGQQAMSLAILR 268
 lLrllrllrrletlfefelgtlaWslqslg.ralksilrfllllllllllig
 ++rl+r++r ++ + +++ lq+lg+++ +s+ ++ll+++l+ig
 12189 269 VIRLVRFVRIFKLSR---HSGK---LQILGqTLRASMRELGLLIFFLFIG 312
 fsvigyllfkgyedlsenevdgnsefssyfdafyflfvltttvGfGdlvp
 + +++ +++++ + d+ +s f+s++++f++++vt+ttvG+Gd+ p
 12189 313 VVLFSsAVYFAEVDV-----DSHFTSIPESFWWAVVTMTTVGYGDMAP 356
 v.wlgiiffvlfiiivgllllnlliavi<-*
 v+++g+i++ ++++i+g+l+++l+++vi
 12189 357 VtVGGKIVG-SLCAIAGVLTISLPVPVI 383

Figure 6B

Mouse Kv1.7
(SEQ ID NO:13)
12189

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MTTRKAQEIH GKAPGGSVST GVGTAEGAPS PAGVTPPPPP R_PGRTFHAIF
.....

TRRHRTPDWG GCGVGATRPF TGRPGCARHG ATVPAALRCC ERLVLNVAGL
.....CC ERLVLNVAGL

RFETRARTLG RFPDTLLGDP VRRSRFYDGA RAEYFFDRHR PSFDAVLYYY
RFETRARTLG RFPDTLLGDP ARRGRFYDDA RREYFFDRHR PSFDAVLYYY

QSGGRLRRPA HVPLDVFL EE VSFYGLG.RR LARLREDEGC AVA.ERPLPP
QSGGRLRRPA HVPLDVFL EE VAFYGLGAAA LARLREDEGC PVPPERPLPR

.PFARQLWLL FEFPESSQAA RVLAVVSVLV ILVSIVVFCL ETLPDFRDDR
RAFARQLCLL FEFPESSQAA RVLAVVSVLV ILVSIVVFCL ETLPDFRDDR

DDPGLAPVAA ATGSFLARLN GSSPM PGAPP RQPFNDPFFV VETLCICWFS
DGTGLA.AAA AAGPFPAPLN GSSQMPGNPP RLPFNDPFFV VETLCICWFS

FELLVHLVAC PSKAVFFKNV MNLIDFVAIL PYFVALGTEL ARQRGVGQPA
FELLVRLVC PSKAIFFKNV MNLIDFVAIL PYFVALGTEL ARQRGVGQQA

MSLAILRVIR LVRVFRIFKL SRHSKGLQIL GQTLRASMRE LGLLIFFLFI
MSLAILRVIR LVRVFRIFKL SRHSKGLQIL GQTLRASMRE LGLLIFFLFI

GVVLFSSAVY FAEVDRVDTH FTSIPESFWW AVVTMTTVGY GDMAPVTVGG
GVVLFSSAVY FAEVDRVDSH FTSIPESFWW AVVTMTTVGY GDMAPVTVGG

KIVGSLCAIA GVL TISLPVP VIVSNFSYFY HRETEGEEAG MYSHVDTQPC
KIVGSLCAIA GVL TISLPVP VIVSNFSYFY HRETEGEEAG MFSHVDMQPC

GTLEGKANGG LVDSEVPELL PPLWPPAGKH MVTEV
GPLEGKANGG LVDGEVPELP PPLWAPPGKH LVTEV

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Figure 6C

0987654321060504